

APPENDIX B: AMINO ACID SEQUENCES

> RXA00315 (1-1086, translated) 362 residues
YDFGGPVGGL LFGLVYSPIV ITGLHQSFPF IELELFNQGG SFIFATASMA NIAQGAACLA
VFFLAKSEKL KGLAGASGVS AVLGITEPAI FGVNLRRLWP FFIGIGTAAI GGALIALFNI
KAVALGAAGF LGVVSIDAPD MVMFLVCAVV TFFIAFGAAI AYGLYLVRN GSIDPDATAA
PVPAGTTKAE AEAPAEFSND STIIQAPLTG EAIALSSVSD AMFASGKLGS GVAIVPTKGQ
LVSPVSGKIV VAFPSGHAF VRTKAEDGSN VDILMHIGFD TVNLNGTHFN PLKKQGDVVK
AGELLCEFDI DAIKAAGYEV TPIVVSNYK KTGPVNTYGL GEIEAGANLL NVAKKEAVPA
TP

> RXA00951 (1-393, translated) 131 residues
IQAILKAAA PAKQKAPAVA PAVTPTDAPA ASVQSKTHDK ILTVCGNGLG TSLFLKNTLE
QVFDTWGWP YMTVEATDTI SAKGKAKEAD LIMTSGEIAR TLGDVGIPVH VINDFTSTDE
IDAALRERYD I

> RXA01244 (1-1509, translated) 503 residues
LLERSEAAEG PAEEVLKATA GMVNDRGWRK AVIKGVKGGH PAEYAVVAAT TKFISMFEAA
GGLIAERTTD LRDIRDRVIA ELRGDEEPGL PAVSGQVILF ADDLSPADTA ALDIDLTVGL
VTELGGPTSH TAIARQLNV PCIVASGAGI KDIKSGEKVL IDGSLGTIDR NADEAEATKL
VSESLERAAR IAEWKGAQT KDGVRVQLLA NVQDGNASQQ AAQTEAEGIG LFRTELCLFLS
ATEEPSVDEQ AAVYSKVLEA FPESKVVVRS LDAGSDKPVP FASMADEMNP ALGVRGLRIA
RGQVDLLTRQ LDAIAKASEE LGRGDDAPTW VMAPMVATAY EAKWFADMCER ERGLIAGAMI
EVPAASLMAD KIMPHLDFVS IGTNDLTQYT MAADRMSPEL AYLTDPWQPA VLRLIKHTCD
EGARENTPVG VCGEAAADPL LATVLTGLGV NSLSAASTAL AAVGAKLSEV TLETCKKAAE
AALDAEGATE ARDAVRAVID AAV

> RXA01299 (1-441, translated) 147 residues
MEIMAAIMAA GMVPPIALSI ATLLRKKLFT PAEQENGKSS WLLGLAFVSE GAIPFAAADP
FRVIPAMMAG GATTGAISMA LGVGSRAHPG GIFVVWAIEP WWGWLIALLA GTIVSTIVVI
ALKQFWPNKA VAAEVAKQEA QQAAVNA

> RXA01300 (1-267, translated) 89 residues
MASKTVTVGS SVGLHARPAS IIAEAAAEDY DEILLTLVGS DDDEETDASS SLMIMALGAE
HGNEVTVTSD NAEAVEKIAA LIAQDLDAE

> RXA01503 (1-249, translated) 83 residues
MFLAVILAIT AARKFGANVF TSVALAGALL HTQLQAVTVL VDGLQSMSTL VAFQKAGNDV
TFLGIPVVLQ LALHVASLMK LSR

> RXA01883 (1-480, translated) 160 residues
MNSVNNSSLV RLDVDFGDST TDVINNLATV IFDAGRASSA DALAKDALDR EAKSGTGVPG
QVAIPHCRSE AVSVPTLGFA RLSKGVDFSG PDGDANLVFL IAAPAGGGKE HLLKLSKLAR
SLVKKDFIKA LQEATTEQEI VDVVDAVLNP APKNHRASCS

> RXA01889 (1-555, translated) 185 residues
VAITACPTGI AHTYMAADSL TQNAEGRDDV ELVVETQGSS AVTPVDPKII EAADAVIFAT
DVGVKDRERF AGKPVIESGV KRAINEPAKM IDEAIAASKN PNARKVSGSG VAASAETTGE
KLGWGKRIQQ AVMTGVSYMV PFVAAGGLLL ALGFAFGGYD MANGWQAIAT QFSLTNLPGN
TVDVD

> RXA01943 (1-405, translated) 135 residues
PDPIFAAGKL GPGIAIQPTG NTVVAPADAT VILVQKSGHA VALRLDSGVE ILVHVGLDTV
QLGGEGFTVH VERRQVKGAG DPLITFDADF IRSKDLPLIT PVVVSNAAKF GEIEGIPADQ
ANSSTTVIKV NGKNE

> RXA02191 (1-1239, translated) 413 residues
MASKLTTTSQ HILENLGGPD NITSMTHCAT RLRQVQKQDS IVDQQEIDSD PSVLGVVPQG
STGMQVVMGG SVANYQEIL KLDGMKHFAD GEATESSSKK EYGGVRGKYS WIDYAFEFLLS
DTRFPIWLAL LGASLIITLL VLADTFGLQD FRAPMDEQPD TYVFLHSMWR SVFYFLPIMV
GATAARKLGA NEWIGAAIPA ALLTPEFLAL GSAGDTVTVF GLPMVLNDYS QGVFPPLIAA

IGLYWVEKGL KKIIEAVQM VFVPPFSLI MIPATAFLLG PFGIGVNGI SNLLEAINNF
SPFILSIVIP LLYPFLVPLG LHWPLNAIMI QNINTLGYDF IQGPMGAWN ACFLVLTGVF
LLSIKERNKA MRQVSLGGML AGLLGGISEP SLYGVLLRFK KTYFRLLPGC LA

>RXN01244 TRANSLATE of: rxn01244.seq check: 8583 from: 1 to: 1704
VATVADVNDQTVLKGTGVVGGVRYASAVWITPRPELPQAGEVVAEENREAEQERFDAAAA
TVSSRLLEERSEAAEGPAAEVLKATAGMVNDRGWRKAVIKGVKGGHPAEYAVVAATTKFIS
MFEAAGGLIAERTTDLRDIRDVIAELRGDEEPGLPAVSGQVILFADDLSPADTAALDTD
LFVGLVTELGGPTSHTAIARQLNVPCIVASGAGIKDIKSGEKVLIDGSLGTIDRNDADA
EATKLVSESLERAARIAEWKGAQTKDGYRVQLLANVQDGNASQAQAQTEAEGIGLFRTE
LCFLSATEEPSVDEQAAYVSKVLEAFPEKVVVRSLDAGSDKPVFASMADEMNPALGVR
GLRIARGQVDLLTRQLDAIAKASEELGRGDDAPTWMAPMVATAYEAKWFADMCRRGLI
AGAMIEVPAASLMADKIMPHLDFVSIQNTDLTQYTMADRMSPELAYLTPWQPAVLRRI
KHTCDEGARFNTPVGVCGEAAADPLLATVLTGLGVNSLSAASTALAAVGAKLSEVTLETC
KKAEEAALDAEGATEARDAVRAVIDAAV

>RXN01299 TRANSLATE of: rxn01299.seq check: 4359 from: 1 to: 2064
MNSVNNSSLVRLDVFDDSTTDVINNLATVIFDAGRASSADALAKDALDREKSGTGVP
QVAIPHCRSEAVSVPTLGFARLSKGVDFSGPDGDANLVFLIAAPAGGGKEHLKILSKLAR
SLVKKDFIKALQEATTEQEIVDVVDAVLNPAPKTTEPAAAPAAAABAESGAASTSVTRIV
AITACPTGIAHTYMAADSLTQNAEGRDDVELVETQGSASVTPVDPKIIAADAVIDFATD
VGVKDRERFAGKPVIESGVKRAINEPAKMIIDEAIAASKNPNARKVSGSGVAASAETTGEK
LGWKGRIQQAVMTGVSVMVFFVAAGGLLLALGFAFGGYDMANGWQAIATQFSLTNLPNT
VDVDGVAMTFERSGFLLYFGAVLFATGQAAMGFIVAALSGYTAYALAGRPGIAPGFVGG
ISVTIGAGFIGGLVTGILAGLIALWIGSWKVPVQSLMPVVIIPLLTSVVVGLVMYLL
GRPLASIMTGLQDWLSSMSGSSAILLGIILGLMMCFDLGGPVNKAAYLFGTAGLSTGDA
SMEIMAAIMAAGMVPPIALSIAITLLRKKLFTPAEQENGKSSWLLGLAFVSEGAIPFAAAD
PFRVIPAMMAGGATTGAISMALGVSRAPHGGIFVVAIEPWWGWLIALAAGTIVSTIV
IALKQFWPNKAVAAEVAKQEAQQAANA

>RXN01943 TRANSLATE of: rxn01943.seq check: 1650 from: 1 to: 2049
MASKLTTSQHILENLGGPDNITSMTHCATRLRFQVKDQSIVDQOEIDSDPSVLGVVPQ
STGMQVVMGGSVANYQEIILKLDGMKHFADGEATESSSKKEYGGVRGKYSWIDYAFEF
DTRFPIWLWLGASLIITLLVLADTFGLQDFRAPMDEQPDYVFLHSMWRSVYFPLIMV
GATAARKLGANEWIGAAIPAAALLTPEFLALGSAGDTVTVFGPLMVLNDYSGQVFPPLIA
IGLYWVEKGLKKIIEAVQMVFVPPFSLIMIPATAFLLGPFPGIGVNGISNLLEAINNF
SPFILSIVIPLLYPFLVPLGLHWPNAIMIQNINTLGYDFIQGPMGAWNACFLVLTGVF
LLSIKERNKAMRQVSLGGMLAGLLGGISEPSLYGVLLRFKKTFRLLPGCLAGGIVMGIF
DIKAYAFVFTSLTIIPAMDPWLGYTIGIAVAFFVSMFLVLALDYRSNEERDEARAKVAAD
KQAEEDLKAEANATPAAPVAAAGAGAGAGAGAAAGAATAVAAPKLAAGEVVDIVSPLEG
KAIPLEVPDPIFAAGKLGPGLIAIQPTGNTVVAPADATVILVQKSGHAVALRLDSGVEIL
VHVGLDVTQLGGEFTVHVRRQOVKAGDPLITFDADFIRSKDLPLITPVVVSNAAKFGE
IEGIPADQANSSTTVIKVNGKNE

>RXN03002 TRANSLATE of: rxn03002.seq check: 5800 from: 1 to: 408
MFVLKDLLKAERIELDRTVTDWREGIRAAGVLEKTNSIDSAYTDAMIASVEEKGPYIVV
APGFATAHARPSRAVRETAMSWVRLASPVSGHKNLPLNLIVALAAKDATAHTQAMAAL
AKALGKYRKDLDEAQS

>RXS00315 TRANSLATE of: RXS00315.seq check: 1474 from: 1 to: 1404
MAMVFPVSLVNGYDVAATMAAGEMPMSLFLGLDVAQAGYQGTVPVVLVSWILATIEKFLHKRLKGTADF
LITPVLTLTLTGFLTIFIAIGPAMRWGDVLAHGLQGLYDFGGPVGGLLFGLVYSPIVITGLHQSFPPIE
LELFNQGSFIFATASMANIAQGAACLAFFLAKSEKLKGLAGASGVSALVGITEPAIFGVNLRRLRWP
FIGIGTAAIGGALIALFNKAVALGAAGFLGVVSDAPDMVMFLVCAVVTFFIAFGAAIAYGLYLVRN
GSIDPDATAAPVPAGTTKAEAEAPAEFSNDSTIIQAPLTGEAIALSSVSDAMFASGKLGSGVAIVPTKG
QLVSPVSGKIVVAFPSGHAFVVRTKAEDGSNDILMHIGFDTVNLNGTHFNPLKKQGDEVKAGELLCEF
DIDAIKAAGYEVTTPIVVSNYKKTGPVNTYGLGEIEAGANLLNVAKKEAVPATP

>RXC00953 TRANSLATE of: RXC00953.seq check: 8687 from: 1 to: 753

MAPPTVGN YIMQSFTQGLQFGVAVAVILFGVRTILGELVPAFQGI AAKVVPGAI PALDAPIVFPYAQNA
VLIGFLSSFVGGGLVGLTVLASWLNPAFGVALILPGLVPHFFTGGAAGVYGNATGGRRGAVFGAFANGLL
ITFLPAFLLGVLGSFGSENTTFGDADFGWFGIVVGSAAKVEGAGGLILLIIAAVLLGGAMVFKRVVN
GHWDPAPNRERVEKAEADATPTAGARTYPKIAFPAGAPTTPARS

>RXC03001 TRANSLATE of: RXC03001 .seq check: 9853 from: 1 to: 453
MDWLTIPFLVNEILAVPAFLIGIITAVGLGAMGRSVGVIGGAIKATLGFLIGAGATLV TASLEPLG
AMIMGATGMRGVVPTNEAIA GIAQA EYGAQVAWLMILGFAISLVLARFTNLRYVLLNGHHVLLMCTMLT
MVLATGRVDAWIF

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